AMENDMENT TO THE SPECIFICATION

The last paragraph on page 4 and continuing on page 5 has been amended as follows:

Within the context of the present invention alignment are conveniently performed using BLAST, a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. Version BLAST 2.0 (Gapped BLAST) of this search tool has been made publicly available ~~www.ncbi.nlm.nih.gov/BLAST/>~~). It uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions. The scores assigned to a BLAST search have a well-defined statistical interpretation. Particularly useful within the score of the present invention are the blastp program allowing for the introduction of gaps in the local sequence alignments and the PSI-BLAST program, both programs comparing an amino acid query sequence against a protein sequence database, as well as a blastp variant program allowing local alignment of two sequences only. Said programs are preferably run with optional parameters set to the default values.

The Abstract has been amended as follows:

ABSTRACT

The present invention relates to DNA that encodes proteins involved in gene silencing, in particularDNA encoding the MOM protein and allelic variants thereof from *Arabidopsis thaliana*, as well as to the use of such DNA in releasing transcriptional gene silencing. ~~Related genes encoding proteins characterized by an amino acid sequence comprising a component sequence of at least 150 amino acid residues having 40% or more identity with an aligned component sequence of SEQ ID NO 3 can be isolated from different sources such as mammalian or plant cells. Further disclosed is a method for isolating DNA according to the invention.~~